CLAIMS

1. A method for detecting replication of severe acute respiratory syndrome coronavirus (SARS-coronavirus) in a sample, comprising detecting the presence SARS-coronavirus subgenomic RNA in a sample by reverse transcriptase polymerase chain reaction (PCR).

2. The method of Claim 1, wherein said subgenomic RNA comprises at least a portion of a leader sequence.

3. The method of Claim 1, further comprising detecting SARS-coronavirus genomic RNA.

4. The method of Claim 1, further comprising detecting SARS-coronavirus polypeptide or particles.

5. The method of Claim 3, comprising using a sense primer set forth as SEQ ID NO:90, an antisense primer set forth as SEQ ID NO:89, and a second antisense primer set forth as SEQ ID NO:88, for simultaneously detecting said SARS-coronavirus subgenomic RNA and genomic RNA in a sample.

6. A method for detecting the presence of severe acute respiratory syndrome coronavirus (SARS-coronavirus) in a sample, comprising:

a) providing:

(i) a sample; and

(ii) cells, wherein said cells support replication of SARS-coronavirus in the absence of substantial cytopathic effect;

b) inoculating said cells with said sample to produce inoculated cells; and

c) detecting the presence of said SARS-coronavirus in said inoculated cells.

7. The method of Claim 7, wherein said detecting comprises detecting the presence of subgenomic RNA.

8. The method of Claim 6, wherein said detecting comprises detecting the presence of SARS-coronavirus genomic RNA.

9. The method of Claim 6, wherein said detecting comprises detecting the presence of a SARS-coronavirus polypeptide.

10. The method of Claim 6, wherein said cells comprise a transgenic cell.

11. The method of Claim 10, wherein said transgenic cell comprises a transgenic mink lung epithelial cell line expressing human furin, wherein said cell line has a property chosen from (a) increased sensitivity to at least one virus selected from the group consisting of influenza A virus, influenza B virus and parainfluenza virus 3, as compared to Mv1Lu, and (b) enhanced productivity of infectious virions upon inoculation with a virus chosen from influenza A virus, influenza B virus and parainfluenza virus 3, as compared to Mv1Lu.

12. The method of Claim 6, wherein said cells are chosen from HEK-293T, Huh-7, Mv1Lu, pRHMK and pCMK.

13. The method of Claim 6, wherein said cells are in single cell type culture.

14. The method of Claim 6, wherein said cells are in mixed cell type culture with a second cell type.

15. The method of Claim 6, wherein said cells are frozen *in situ*

16. The method of Claim 6, wherein said sample is isolated from a mammal.

17. The method of Claim 6, wherein said mammal is human.

18. A method for detecting the presence of severe acute respiratory syndrome coronavirus (SARS-coronavirus) in a first sample and in a second sample, comprising:

a) providing:

(i) a first sample;

(ii) a second sample;

b) contacting test cells with:

(i) said first sample to produce a first treated sample; and

(ii) said second sample to produce a second treated sample;

wherein said test cells support replication of SARS-coronavirus in the absence of substantial cytopathic effect, and said contacting is such that said test cells are infected with SARS-coronavirus;

c) detecting the presence of SARS-coronavirus genomic RNA and SARS-coronavirus subgenomic RNA in said first treated sample and said second treated sample, wherein said detecting indicates the presence of said SARS-coronavirus in said first treated sample and said second treated sample.

19. The method of Claim 18, wherein said detecting comprises detecting an absence of SARS-coronavirus subgenomic RNA in said first treated sample.

20. The method of Claim 18, wherein said detecting comprises detecting a reduced level of SARS-coronavirus subgenomic RNA in said first treated sample compared to the level of subgenomic RNA in said second treated sample.

21. The method of Claim 18, wherein said detecting comprises detecting a reduced ratio of SARS-coronavirus subgenomic RNA level to SARS-coronavirus genomic RNA level in said first treated sample compared to said ratio in said second treated sample.

22. The method of Claim 18, wherein said first sample and said second sample are isolated from a mammal.

23. The method of Claim 18, wherein said test cells are chosen from HEK-293T, Huh-7, Mv1Lu, pRHMK and pCMK.

24. A method for identifying a test agent as altering replication of severe acute respiratory syndrome coronavirus (SARS-coronavirus) in a cell, comprising:

a) providing cells treated with a first test agent, wherein said cells support replication of SARS-coronavirus in the absence of substantial cytopathic effect; and

b) detecting an altered level of replication of SARS-coronavirus in cells treated with said first test agent compared to a level of replication of SARS-coronavirus in cells not treated with said first test agent, wherein said detecting identifies said first test agent as altering replication of SARS-coronavirus in a cell.

25. The method of Claim 24, wherein said altered level is a reduced level.

26. The method of Claim 24, wherein said altered level is an increased level.

27. The method of Claim 24, wherein said detecting comprises detecting SARS-coronavirus subgenomic RNA.

28. The method of Claim 24, wherein said detecting comprises detecting SARS-coronavirus genomic RNA.

29. The method of Claim 24, wherein said detecting comprises detecting SARS-coronavirus polypeptide or particles.

30. The method of Claim 24, wherein said cells are chosen from HEK-293T, Huh-7, Mv1Lu, pRHMK and pCMK.

31. The method of Claim 24, wherein said detecting comprises detecting an absence of SARS-coronavirus genomic RNA in said cells treated with said first test agent.

32. The method of Claim 24, wherein said detecting comprises detecting a reduced level of SARS-coronavirus subgenomic RNA in said cells treated with said first

test agent compared to the level of SARS-coronavirus subgenomic RNA in said cells that are not treated with said first test agent.

33. The method of Claim 32, wherein detecting an increased reduction in the level of SARS-coronavirus subgenomic RNA in said cells treated with said first test agent compared to said cells treated with a second test agent identifies said first test agent as more efficacious than said second test agent in reducing replication of SARS-coronavirus in a cell.

34. The method of Claim 24, wherein said detecting comprises detecting a reduced ratio of SARS-coronavirus subgenomic RNA level relative to SARS-coronavirus genomic RNA level in said cells treated with said first test agent compared to said ratio in said cells that are not treated with said first test agent.

35. The method of Claim 34, wherein detecting an increased reduction in said ratio of SARS-coronavirus subgenomic RNA level to SARS-coronavirus genomic RNA level in said cells treated with said first test agent compared to said ratio in said cells treated with a second test agent identifies said first test agent as more efficacious than said second test agent in reducing replication of SARS-coronavirus in a cell.

36. An antibody specific for one or more SARS-coronavirus antigen that is produced by a cell chosen from HEK-293T, Huh-7, Mv1Lu, and pRHMK.

37. The antibody of Claim 36, wherein said antibody is a polyclonal antibody.

38. The antibody of Claim 36, wherein said antibody is a monoclonal antibody.

39. The antibody of Claim 36, wherein said antibody is a humanized antibody.

40. A composition comprising: (i) cells susceptible to a virus that is not a plus-strand RNA virus, and (ii) protease inhibitor.

41. A method for detecting a virus that is not a plus-strand RNA virus in a sample, comprising:

a) providing:

i) a sample;

ii) cells susceptible to said virus that is not a plus-strand RNA virus; and

iii) at least one protease inhibitor;

b) contacting said cells and said sample in the presence of said protease inhibitor to produce contacted cells, wherein replication of said virus that is not a plus-strand RNA virus in said contacted cells is not reduced relative to replication of said virus that is not a plus-strand RNA virus in cells not contacted with said protease inhibitor, and wherein replication of a plus-strand RNA virus in said cells contacted with said protease inhibitor is reduced relative to replication of said plus-strand RNA virus in cells not contacted with said protease inhibitor.

42. The method of Claim 41, wherein said virus that is not a plus-strand RNA virus is chosen from influenza virus, parainfluenza virus, adenovirus, respiratory syncytial virus, and metapneumovirus.

43. The method of Claim 42, wherein said influenza virus is chosen from influenza A, influenza B, and influenza C.

44. The method of Claim 42, wherein said parainfluenza virus is chosen from parainfluenza 1, parainfluenza 2, parainfluenza 3, and parainfluenza 4.

45. The method of Claim 42, wherein said adenovirus is chosen from adenovirus 2, adenovirus 3, adenovirus 4, adenovirus 5, adenovirus 7, adenovirus 9, adenovirus 12, adenovirus 17, and adenovirus 40.

46. The method of Claim 41, wherein said plus-strand RNA virus is chosen from togavirus, flavivirus, coronavirus, and picornavirus.

47. The method of Claim 46, wherein said coronavirus comprises SARS-coronavirus.

48. A method for detecting replication of a coronavirus in a sample, comprising detecting the presence of coronavirus subgenomic RNA in a sample by reverse transcriptase polymerase chain reaction (PCR).

49. The method of Claim 48, wherein said subgenomic RNA comprises at least a portion of a leader sequence.

50. The method of Claim 49, further comprising detecting coronavirus genomic RNA in said sample.

51. The method of Claim 48, wherein said coronavirus is chosen from human coronavirus 229E, human coronavirus OC43, and mouse hepatitis virus.

52. The composition of Claim 40, further comprising a cyclodextrin.

53. The composition of Claim 52, wherein said cyclodextrin is Captisol.

54. The composition of Claim 53, wherein said protease inhibitor is selected from Actinonin, Glycyrrhizin, and E64D.

55. A method for inhibition of human coronavirus 229E replication comprising: i) providing a composition comprising the protease inhibitor E64D and Captisol; and ii) contacting a cell permissive for 229E replication with said composition under conditions suitable for inhibiting 229E replication in said cell.

56. A kit for detecting replication of a coronavirus in a sample, comprising providing:

i) at least two coronavirus primers comprising a sense primer and an antisense primer; and

ii) instructions for using said primers for detecting coronavirus subgenomic RNA in a sample by reverse transcriptase polymerase chain reaction (RT-PCR).

57. The kit of Claim 56, further comprising providing cells susceptible for infection by a coronavirus, and instructions for using said cells for propagation of a coronavirus in a sample.

58. Th kit of Claim 56, wherein said sense primer anneals to a coronavirus leader cDNA sequence, and said antisense primer anneals to a coronavirus coding cDNA sequence.

59. The kit of Claim 58, further comprising providing a second sense primer, wherein said second sense primer anneals to a coronavirus coding cDNA sequence for simultaneously detecting coronavirus genomic RNA in a sample by RT-PCR.

60. The kit of Claim 56, wherein said coronavirus is a severe acute respiratory syndrome (SARS) coronavirus.

61. The kit of Claim 60, wherein said sense primer is set forth as SEQ ID NO:76, said antisense primer is set forth as SEQ ID NO:75, and said second antisense primer is set forth as SEQ ID NO:74.

62. The kit of Claim 56, wherein said coronavirus is human coronavirus 229E.

63. The kit of Claim 62, wherein said sense primer is set forth as SEQ ID NO:90, said antisense primer is set forth as SEQ ID NO:89, and said second antisense primer is set forth as SEQ ID NO:88.

64. The kit of Claim 56, wherein said cornonavirus is human coronavirus OC43.

65. The kit of Claim 64, wherein said sense primer is set forth as SEQ ID NO:96, said antisense primer is set forth as SEQ ID NO:95, and said second antisense primer is set forth as SEQ ID NO:94.

66. The kit of Claim 56, wherein said coronavirus is mouse hepatitis virus.

67. The kit of Claim 66, wherein said sense primer is set forth as SEQ ID NO:93, said antisense primer is set forth as SEQ ID NO:92, and said second antisense primer is set forth as SEQ ID NO:91.